



Title: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
IMPAIRED GLUCOSE TOLERANCE CONDITIONS

Applicants: Gary Ruvkun et al.

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Comparison of the human AKT protein sequence to the cosmid sequence
C12D8, located in the genetic interval where sup(mg144) maps. Numbering in the AKT
protein sequence by amino acid residues, and in the cosmid sequence by nucleotide
position.

Score = 450 (207.4 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 79/121 (65%), Positives = 97/121 (80%), Frame = +1

SEQ ID No: 87 Query: 319 EVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKS 378
SEQ ID No: 325 +VL+D+DYGR VDWVG+GVVMYEMMCGRLPFY++DH KLFELI+ ++RFP L EA++
SEQ ID No: 88 Sbjct: 33685 QVLDDHDYGRCDVWVGWGVVMYEMMCGRLPFYSKDHNKL FELIMAGDLRFP SKLSQEART 33864

Query: 379 LLSGLLKKDPTQRLGGGSEDAKEIMQHRFFANIVWQDVYEKKLSPPFKPQVTSSETDTRYFD 439
LL+GLL KDPTQRLGGG EDA EI + FF + W+ Y K++ PP+KP V SETDT YFD
Sbjct: 33865 LLTGLLVKDPTQRLGGGPEDALEICRADFPRTVDWEATYRKEIEPPYKPNVQSETDTSYFD 34047

Score = 256 (118.0 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 48/66 (72%), Positives = 59/66 (89%), Frame = +1

SEQ ID No: 89 Query: 146 TMNEFEYLKLLGKGTFGKVILVKEKATGRYAMKILKKEVIVAKDEVAHTLTENRVLQNS 205
SEQ ID No: 326 TM +F++LK+LGKGTFGKVIL KEK T + YA+KILKK+VI+A++EVAHTLTENRVLQ
SEQ ID No: 90 Sbjct: 32314 TMEDFDPLKVLGKGTFGKVILCKEKRTQKLYAIKILKDVIIAREEVAHTLTENRVLQRC 32493

Query: 206 RHPFLT 211
+HPFLT
Sbjct: 32494 KHPFLT 32511

Score = 190 (87.6 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 36/45 (80%), Positives = 37/45 (82%), Frame = +2

SEQ ID No: 91 Query: 276 KLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEV 320
SEQ ID No: 99 KLENL+LDKDGHIKI DFGLCKE I G TFCGTPEYLAPEV
SEQ ID No: 92 Sbjct: 33509 KLENLLLDKDGHIKIADFGLCKEISFGDKTSTFCGTPEYLAPEV 33643

Score = 188 (86.7 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 37/57 (64%), Positives = 42/57 (73%), Frame = +3

SEQ ID No: 93 Query: 209 FLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAETVSALDY LH 265
SEQ ID No: 100 + LKYSFQ LCFVM++ANGGELF H+ + PSE RARFYGAETV AL YLH
SEQ ID No: 94 Sbjct: 32667 YFQELKYSFQEQHYLCFVMQFANGGELFTHVRKCGTFSEPRARFYGAETV LALGYLH 32837

Score = 166 (76.5 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 29/59 (49%), Positives = 42/59 (71%), Frame = +1

SEQ ID No: 95 Query: 53 NNFSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHVETPEEREWEATAIQTVADGLK 111
SEQ ID No: 101 + F++ Q M E+PRPN F++RCLQWTTVIERTF+ E+ E R+ W AI++++ K
SEQ ID No: 96 Sbjct: 31846 STFAIFYFQTM LFEKPRPNMFMVRLQWTTVIERTFYAESAEVRQRWIHAIESISKKYK 32022

Score = 134 (61.8 bits), Expect = 5.2e-167, Sum P(8) = 5.2e-167
Identities = 24/33 (72%), Positives = 30/33 (90%), Frame = +3

SEQ ID No: 97 Query: 210 LTALKYSFQTHDRLCFVMEYANGGELFFHLSRE 242
SEQ ID No: 102 L LKYSFQT+DRLCFVME+A GG+L++HL+RE
SEQ ID No: 98 Sbjct: 33156 LQELKYSFQTNDRLCFVMEFAIGGDLYYHLNRE 33254

Fig. 25